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RAW SEQUENCE LISTING

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Application Serial Number: 10/511,468
Source: PCT
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/511,468

DATE: 01/17/2006
TIME: 11:26:46

Input Set : A:\2005-11-21 4614-0159PUS1.ST25.txt
Output Set: N:\CRF4\01172006\J511468.raw

5 <110> APPLICANT: Soren Weis DAHL et al.
7 <120> TITLE OF INVENTION: TRANSLOCATION DEPENDENT COMPLEMENTATION FOR DRUG SCREENING
9 <130> FILE REFERENCE: 4614-0159PUS1
11 <140> CURRENT APPLICATION NUMBER: US 10/511,468
12 <141> CURRENT FILING DATE: 2004-10-18
14 <160> NUMBER OF SEQ ID NOS: 99
16 <170> SOFTWARE: PatentIn version 3.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 238
20 <212> TYPE: PRT
21 <213> ORGANISM: Aequorea victoria
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28 20 25 30
30 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
31 35 40 45
33 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
34 50 55 60
36 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
37 65 70 75 80
39 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
40 85 90 95
42 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
43 100 105 110
45 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
46 115 120 125
48 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
49 130 135 140
51 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
52 145 150 155 160
54 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
55 165 170 175
57 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
58 180 185 190
60 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
61 195 200 205
63 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
64 210 215 220
66 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
67 225 230 235
69 <210> SEQ ID NO: 2

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70 <211> LENGTH: 238
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79 20 25 30
81 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
82 35 40 45
84 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
85 50 55 60
87 Ser Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
88 65 70 75 80
90 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
91 85 90 95
93 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
94 100 105 110
96 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
97 115 120 125
99 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
100 130 135 140
102 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
103 145 150 155 160
105 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
106 165 170 175
108 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
109 180 185 190
111 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
112 195 200 205
114 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
115 210 215 220
117 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
118 225 230 235
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129 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
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132 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
133 35 40 45
135 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
136 50 55 60
138 Ser His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
139 65 70 75 80

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141 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
142 85 90 95
144 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
145 100 105 110
147 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
148 115 120 125
150 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
151 130 135 140
153 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
154 145 150 155 160
156 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
157 165 170 175
159 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
160 180 185 190
162 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
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183 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
184 35 40 45
186 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
187 50 55 60
189 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
190 65 70 75 80
192 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
193 85 90 95
195 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
196 100 105 110
198 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
199 115 120 125
201 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
202 130 135 140
204 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
205 145 150 155 160
207 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
208 165 170 175
210 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
211 180 185 190

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213 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
214 195 200 205
216 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
217 210 215 220
219 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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222 <210> SEQ ID NO: 5
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224 <212> TYPE: PRT
225 <213> ORGANISM: Aequorea victoria
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231 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
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234 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
235 35 40 45
237 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
238 50 55 60
240 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
241 65 70 75 80
243 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
244 85 90 95
246 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
247 100 105 110
249 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
250 115 120 125
252 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
253 130 135 140
255 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
256 145 150 155 160
258 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
259 165 170 175
261 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
262 180 185 190
264 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
265 195 200 205
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275 <212> TYPE: PRT
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282 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

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283 20 25 30
 285 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 286 35 40 45
 288 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 289 50 55 60
 291 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 292 65 70 75 80
 294 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 295 85 90 95
 297 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 298 100 105 110
 301 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 302 115 120 125
 304 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 305 130 135 140
 307 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 308 145 150 155 160
 310 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 311 165 170 175
 313 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 314 180 185 190
 316 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
 317 195 200 205
 319 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
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 332 <221> NAME/KEY: CDS
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 340 gcc aac aag aag gag ctg gcc cag ctg aag tgg gag ctg cag gcc ctg 95
 341 Ala Asn Lys Lys Glu Leu Ala Gln Leu Lys Trp Glu Leu Gln Ala Leu
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 351 <213> ORGANISM: Homo sapiens
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VERIFICATION SUMMARY

PATENT APPLICATION: **US/10/511,468**

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Input Set : **A:\2005-11-21 4614-0159PUS1.ST25.txt**

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